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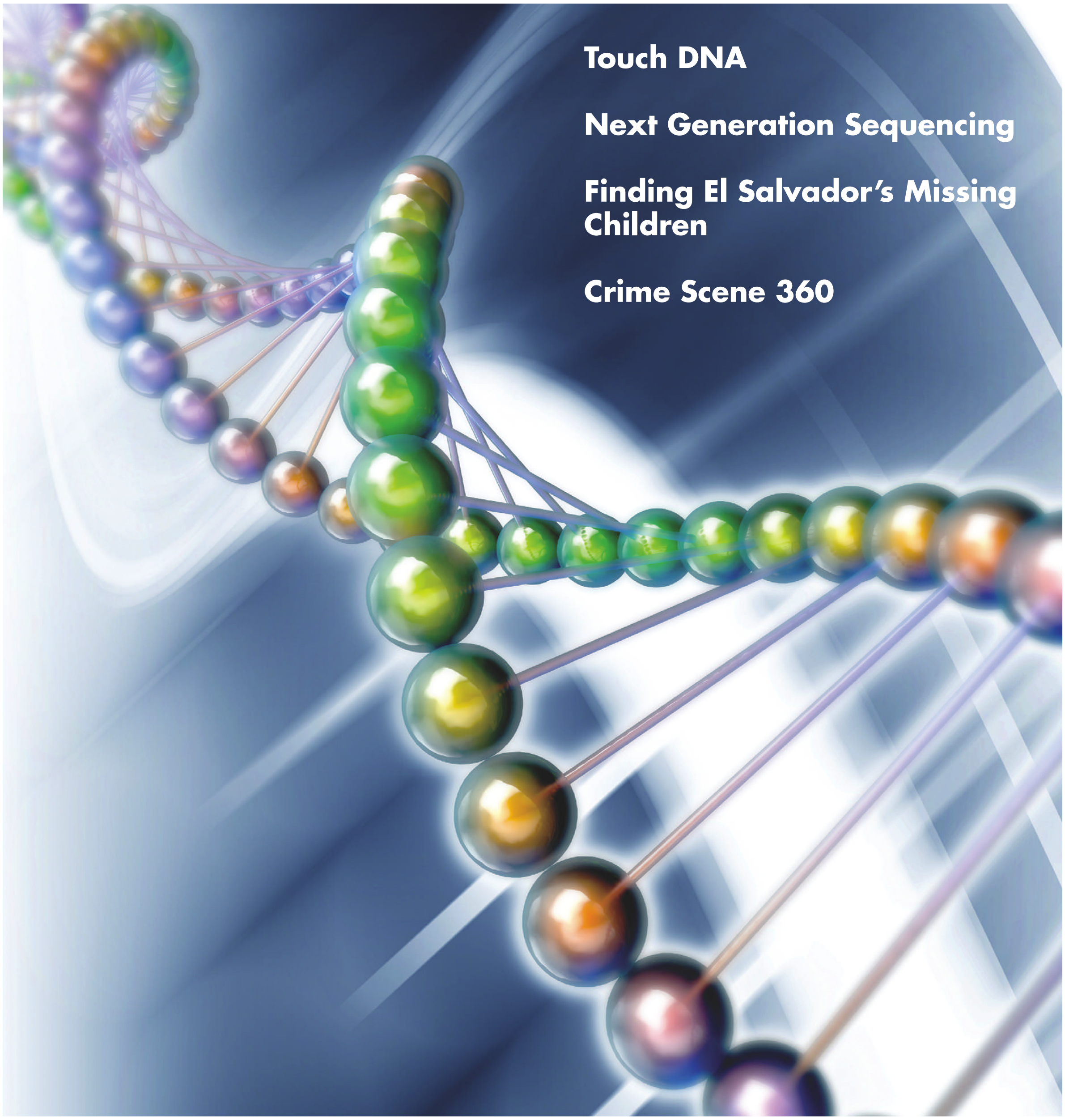

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POSTMASTER: Send return address changes to Forensic Magazine, P.O. Box 3574, Northbrook, IL 60065. Publication Mail Agreement No. 41336030. Return undeliverable Canadian addresses to: Imex/Pitney Bowes, P.O. Box 1632, Windsor Ontario N9A 7C9.
Subscription Inquiries/Change of Address: contact: Omeda Customer Service, P.O. Box 3574, Northbrook, IL 60065-3574, Phone: 847-559-7560, Fax: 847-291-4816, email: abfor@omeda.com. Change of address notices should include old as well as new address. If possible attach address label from recent issue. Allow 8 to 10 weeks for address change to become effective. Subscriptions are free to qualified individuals. Subscription rates per year are $120 for U.S.A., and $180 for Canada, Mexico & foreign air delivery, single copy $15 for U.S.A., $20 for other locations, prepaid in U.S.A. funds drawn on a U.S.A. branch bank.
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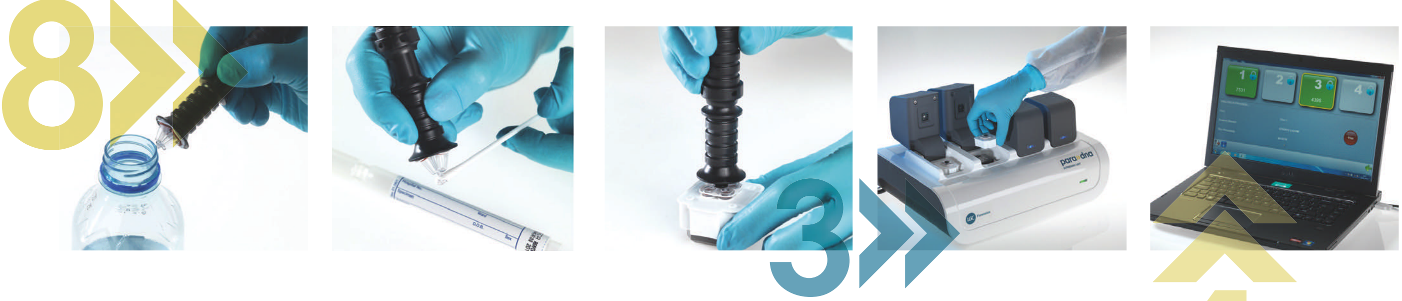

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point of view

David McClure and Kelly A. Walsh

Why Do A Study When I Could Just Tell You?

The value of social science–forensic science partnerships

It's a good question, and one social science researchers in forensic science often hear. We think the answer is simple, but it begins with questions for you: Would you use newly delivered equipment before validating it? Would you allow a new lab examiner to touch casework before being trained and tested? Of course not. It doesn't matter if the new genetic analyzer is the ten thousandth off the line or if the new employee came from the most rigorous academic program. Any assumptions about performance must be tested before you can rely on the results.

The same is true of questions about how forensic labs function within the criminal justice system. How can labs prioritize testing to have the biggest impact on criminal justice outcomes? Is "violent crimes first" always the best policy? How are lab results actually used by law enforcement to aid investigations? Can this be improved? How can you increase transparency on both sides of the adversarial system? Just as with internal lab processes, no one can "just tell you" the answers to these questions. This is the exact reason to "do a study." Have you ever said "Someone really ought to look into that," or "I've been telling people this for years, but no one has been listening to me?" Social scientists working in forensics are the "someones" you should speak to.

As social science researchers, we challenge perceptions of the lab as a black box, where evidence is pumped in and reports are churned out. A quality study can test assumptions, demonstrate cost-effectiveness of lab practices, and build knowledge. Good studies can bridge the gap between lab outputs and untested assumptions about how those outputs help ensure justice.

To Test Assumptions

Untested assumptions abound when it comes to how law enforcement and the courts use forensic science. Labs interact with enforcement, prosecution, defense, accreditation bodies, and state and local stakeholders. At each intersection, criminal justice actors make decisions that can affect the utility of any forensic examination. Decisions based on untested assumptions put valuable resources at risk. For example, we've heard concerns that a portion of lab analyses are completed after the prosecutor has closed a case. Such a practice consumes lab resources while providing no value to the case.

To Demonstrate Cost Effectiveness

A good study can demonstrate cost effectiveness, which can protect

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your budget (sometimes by putting a dollar value on your outputs). Partnering with social scientists on an original research project yields rigorous empirical evaluation of policy or practice. Is it cost effective to send forensic scientists to the crime scene to assist investigators and evidence collectors? Would criminal case court data help you triage cases more efficiently? Independent evaluations of any lab practices, routine or innovative, can answer the question, "Why shouldn't we cut your budget?"

To Build Knowledge

Research on current practices provides evidence to support business as usual, but innovators can also use findings to challenge assumptions and promote evidence-based reform. Part of expanding the evidence base through original research is disseminating that information. Your knowledge as a forensic practitioner may not be shared by the rest of the justice system, or those making decisions about policies and funding. But research provides you information you can use to strengthen the criminal justice field. A social science research proposal may even include resources to put your ideas into action and test whether they produce the intended results.

Social science research in forensics is a young field in a period of exciting growth. Assumptions are no longer enough when making forensic policy and practice decisions. Now we seek to measure the impact of both new and entrenched forensic science policies and practice. What questions will our future work answer? New opportunities are on the horizon as new techniques, policies, and equipment are developed. Each is based on assumptions that it will somehow improve the justice system, but assumptions must be tested.

NIJ's latest Social Science in Forensics solicitation is due May 15, 2013. It is open to all questions, but specifically mentions interest in proposals addressing "sexual assault medical forensic examinations" and "familial DNA searching." We invite the forensics community to join the conversation and partner with social scientists.

David McClure, MA, *and* **Kelly A. Walsh, PhD,** *are research associates with the Justice Policy Center at the Urban Institute. Contact David at DMcClure@urban.org or Kelly at KWalsh@urban.org. The Urban Institute is a nonprofit, nonpartisan policy research and educational organization that examines the social, economic, and governance challenges facing the nation.*

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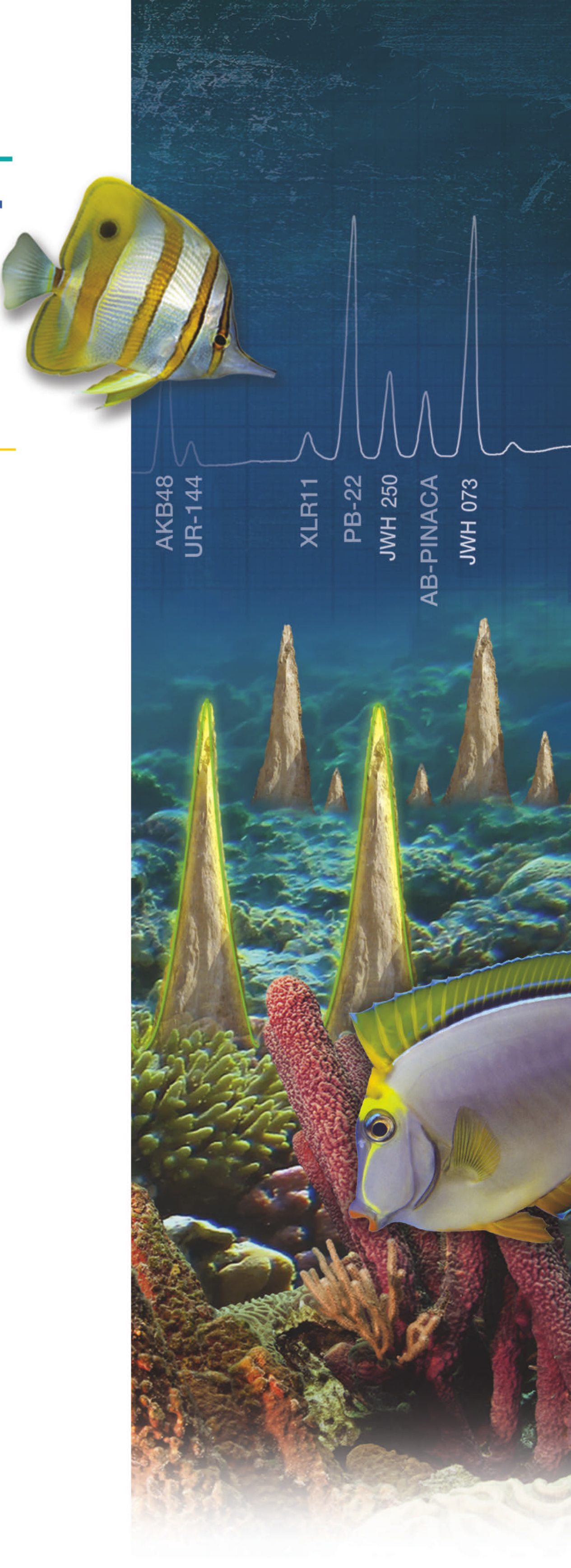

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the dna connection

Chris Asplen

Next Generation Sequencing for Forensics

I was wrong. And I was wrong pretty often. I wasn't the only one; lots of us were out there saying it. Many of us were basing our arguments for expanded databases on it while in official office, under the color of governmental authority. We believed it at the time, and it was a fair basis for argument given what we knew at the time and our view of the future. But those days are over.

The days of arguing that, "We are only looking at these 13 "non-coding" loci." or, "We can't and won't look at anything physical about you etc..." are over. You can't look at the advent of next generation DNA sequencing, the speed at which the technology is advancing, and the rate at which the cost is dropping and—with any intellectual honesty—suggest that the forensic use of DNA is going to continue with blinders to anything phenotypic.

Now if you read this column, even occasionally, you can probably guess that the conclusion of this piece won't be a suggestion that we should stop the pursuit of opportunities presented to us by next gen sequencing. I've never met a forensic DNA application I didn't like and the ability to perform DNA analysis better, faster, and cheaper has always lead to a greater protection of victims and the innocent alike. But I would suggest that, as we move forward, we need to do so with the recognition that some of the issues and objections the law enforcement/forensic community faced with previous methods of DNA analysis may pale in comparison to objections we will face moving forward.

Like every previous advancement in DNA technology, there will be legislative, admissibility, constitutional, and public perception issues. But whatever our previous responses were for the specific changes in technology (the new PCR technique) or application (extending databases to include arrestees), our arguments were always supported by the broader over-arching argument that we weren't even looking into these other areas of the human genome. With NGS we will be doing just that. In the limited information and material on sequencing and forensics, the selling point for the application is just how much information we can glean whereas before, we always argued how little we wanted too. The fact that it is getting faster and cheaper is a bonus.

Whether we are suggesting NGS is a better, cheaper way of getting to the 13 (now 20) core CODIS loci or that gene expression for skin color or eye color is a cost beneficial tool for law enforcement, we as a community need to own the argument in its full and fair context from the beginning.

We only need to look at the debacle that is the national scope—or lack thereof—of our familial searching policies to find a harbinger of things to come. The ill-conceived and uninformed objections to familial searching to fight crime are based on the fact that we are doing more with the 13 core loci than we promised. Objections like, "All family members will become suspects," as ridiculous as they are, gain traction with the uneducated. Years after the FBI issued its memo essentially allowing for familial or close match searching on a state by state basis, some of those states prohibited the use of an amazingly important tool due to a lack of "direction" from the Bureau. That wasn't true. States like Michigan just got it wrong because of a lack of leadership on the issue and blamed the Bureau. When it appeared that the relative of a murderer from Florida might be in the Michigan database, Michigan officials as high as the Governor's office refused to allow the Y-STR testing that would confirm the investigative lead because of "lack of guidance" from the FBI.*

We could easily fail to realize the benefits of sequencing as quickly as we should if, as a community, we don't recognize the concerns that sequencing presents to those who have never trusted government's possession of their genetic identity. As NGS emerges as a technology readily applicable to forensics, we will only leverage its benefits to solve crime and prevent victimization to the extent that we can pave the way for its adoption through solid education and advocacy.

*Note: To its credit, the great state of Michigan under new leadership and continued advocacy by the laboratory and law enforcement recently did perform the Y-STR test at Florida's request. The results did not reveal a connection between the inmate in their system and the unidentified murderer from Florida. An important step in the investigation nonetheless.

Chris Asplen *is President of Asplen and Associates, LLC. He consults with local, state, federal, and international governments on the use of forensic DNA technology. chrisasplen@gmail.com*

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In their DNA: Finding El Salvador's Missing Children

Laura Barten

In El Salvador, the tragic legacy of los desaparecidos—the disappeared—looms large. Beginning in the early 1980s and lasting for more than a decade during the country's bloody conflict years, disappearances were an everyday occurrence. Children were no exception. Kidnapped, separated from their families, a significant number of El Salvador's missing children were illegally placed via suspect agencies with adoptive families the world over. Today, reuniting surviving family members with their loved ones is supported not only by a number of human rights agencies and non-governmental organizations, but also by a small-but-growing group of committed genetic and forensic scientists.

A biochemist, geneticist, and Director of Forensic Programs at the Human Rights Center (HRC) University of California Berkeley School of Law, Cristián Orrego Benavente, Ph.D., has worked for many years on DNA identification and family reunification projects in areas of current and former conflict, including HRC's Building Justice in El Salvador DNA Reunification Project. As part of the Alliance of Forensic Scientists for Human Rights and Humanitarian Investigations, Orrego and his colleagues use kinship analysis to help living relatives who suspect their relatives were illegally placed for adoption during times of instability confirm the identities of individuals who may be among the country's missing. In October 2012, Orrego presented his work during a workshop on forensic science and human rights offered at the 23rd International Symposium on Human Identification (ISHI). To date hundreds have been identified, including 382 missing children from El Salvador, but many more remain unaccounted for and the work continues.

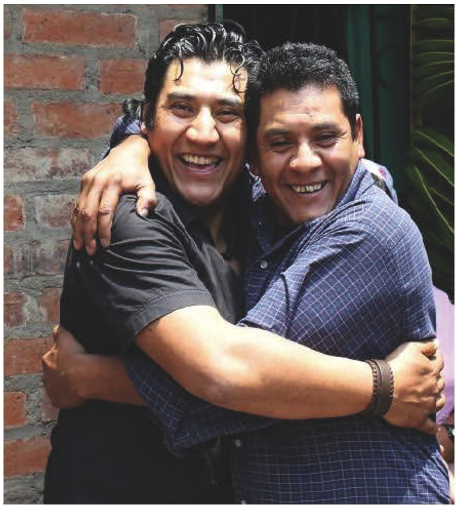

Figure 1: In June 1981, Margarito Ruiz Chácon, age four, was lost during the massacre of Finca Peña in the cantón El Perical, Tecoluca, San Vicente. In 2011, Italian adoptee Eduardo Giai Checco (pictured, left) was confirmed to be Chácon via DNA analysis and reunited with his El Salvadoran family, including his brother (pictured, right).

Tell us about the HRC's Building Justice in El Salvador DNA Reunification Project and its relationship to Pro-Búsqueda in El Salvador.

HRC has been working with Pro-Búsqueda since 2003, helping to develop its ability to use forensic DNA analysis and a robust DNA database to reach more transnational adoptees. Pro-Búsqueda was founded in 1994 by Jon de Cortina, a Roman Catholic Jesuit priest, who lived through the war in El Salvador, including the massacre of 1989 that killed many of his Jesuit brothers. Cortina, with the support of a group of families affected by the conflict, established the Asociación Pro-Búsqueda de Niñas y Niños Desaparecidos, a non-governmental association for the disappeared children of El Salvador, which has existed ever since. This group wanted to organize the search for children that were forcibly separated from their families. During wartime massacres, many of these children perished at the hand of the Salvadoran military units. But other times, they were kidnapped by army personnel, taken to the city, funneled to orphanages, and placed with other families via irregular adoptions, most of which we suspect abroad.

Following in the footsteps of other Latin American non-governmental organizations (NGOs) committed to finding missing persons, Pro-Búsqueda seeks to proactively engage geneticists and forensic professionals to use forensic DNA analysis to identify and reunite some of the missing children with their birth relatives. In El Salvador alone, an estimated 8,000 people went missing between 1980 and 1992 and, as per current Pro-Búsqueda records, close to 500 families were forcibly separated from their children. To date, 382 children have been identified. The work continues, with more than 500 additional missing El Salvadoran children

Figure 2: The delegation from El Salvador, including Cristián Orrego Benavente, Ph.D. (far right), in the headquarters of the ICMP in Sarajevo. Organizations represented included the office of the Ombudsman for Human Rights, the National Search Commission of Missing Children, the Supreme Court of Justice, the Institute for Legal Medicine of the Republic of El Salvador, as well as NGO's Pro-Búsqueda, Tutela Legal del Arzobispado de San Salvador, and Centro para la Promoción de los Derechos Humanos Madeleine Lagadec.

confirmed at large and many families still hopeful they may repeat recent successful matches.

Pro-Búsqueda has been identified as a viable model for other similar organizations. How does the process work? What makes Pro-Búsqueda remarkable is that it is run by a board with representatives from 500 or so member families, and it is one of the few human rights or non-governmental organizations in the world with its own in-house technical expertise. In 2007, with funding HRC received from the State Department Bureau of Democracy, Human Rights, and Labor, Pro-Búsqueda employed a geneticist, who the Alliance of Forensic Scientists helped train in the specialty of kinship analysis via DNA profile comparison. As a result, Pro-Búsqueda has its own DNA database of family profiles to do its work. This effort has had a large payoff. The identification of many individuals was possible only because of DNA analysis. Pro-Búsqueda has some, but not all, adoption records from the civil war period. Yet by connecting names, even via incomplete records, Pro-Búsqueda can sometimes make a connection then use DNA to answer the question "is this child connected to this family in El Salvador?" Often, Pro-Búsqueda doesn't know who the child is, or to what family he or she might belong, and DNA can help provide the answer. A young man in Italy was recently identified in just this way. He knew from his adoptive Italian family that he was adopted from El Salvador when he was four years old, at the beginning of the war. He took a personal interest and traveled to El Salvador to meet with Pro-Búsqueda in 1996, but Pro-Búsqueda was not able to place him at that time. There was no documentation that suggested who he might be. However, several trips later, and following collection of his DNA, a comparison of his DNA profile to the database of families uncovered a link. The power of technology to enhance and speed the investigative process is quite amazing.

Much of this work can be controversial, and may not be supported by the government in question. How did Pro-Búsqueda successfully address roadblocks like this? We've been using a model that has worked very well. In this case, the organization was located in a country that offered no governmental support until very recently. Yet from its inception Pro-Búsqueda was committed to using the scientific tools available in its work to search for children and confirm their kinship to a Pro-Búsqueda family. In 1994, when the organization began the long search for the children of El Salvador, the era of DNA-based human identification was well on its way. Later, when we began the database effort in 2003, we had the good fortune of having qualified forensic geneticist volunteers at the California Department of Justice (CAL DOJ) lab in Richmond, CA, who offered to conduct DNA analysis on the hundreds of samples we were receiving from Pro-Búsqueda. That was the beginning of the Alliance of Forensic Scientists. Then Director of the CAL DOJ DNA

BIENVENIDO
EDUARDO

Figure 3: The Chácon family, reunited.

Lab, Lance Gima was able to obtain permission from the California Office of the Attorney General to have the analysis conducted afterhours and on weekends with funding for reagents and assorted materials for the genetic platforms used in the lab provided by HRC and Physicians for Human Rights in Boston, MA. At the time, we were also fortunate to have forensic mathematician Dr. Charles Brenner join the effort, providing a level of insight and computational capacity into kinship analysis second to none. In short, a remarkable confluence of goodwill and expertise blessed the project from its inception. Subsequently, the generosity of a Phoenix–based commercial lab, Chromosomal Labs Bode Technology (formerly Chromosomal Labs of Phoenix) has sustained us to this day.

We are now fully in our next phase with the accredited DNA lab of Fundación de Antropología de Guatemala (FAFG) in Guatemala City, where Pro-Búsqueda is already processing its samples, bringing the capacity to analyze back to the region. But the important point to be made here is that there is no need to set up DNA analysis capacity in the country in order to make meaningful advances in the search for missing persons. It can be done very well abroad. The transportation of samples is conducted by courier at ambient temperature. Such transportation services are fully accepted for purposes of an unbroken chain of custody. But you must train personnel to know where to send the samples, how to work out the contracts with the labs abroad, and how to receive the data back and acquire the necessary expertise to undertake independent technical review, starting from the "raw" data of the DNA profiles received. This is the training the Alliance of Forensic Scientists has provided for Pro-Búsqueda and its technical personnel since 2003. I think it is a model for other countries without fully installed DNA analysis capacity to consider. It can facilitate a rapid start to an identification effort, particularly when the State is hardly inclined to do so—a situation often found in countries emerging from years of repressive governments and undergoing complicated transitions to democracy. It is possible to undertake a DNA databasing program by training local personnel on the front end and using accredited laboratories abroad on the back end.

What about challenges related to the investigative work itself?
A critical situation that Pro-Búsqueda or any organization doing this work faces: if you arrive too late to the family, many of the closest relatives have died. For many Pro-Búsqueda families, we have only one or two samples and not always the father or mother. This is one reason why we need additional genetic markers, which are coming about now. The International Commission on Missing Persons (ICMP) in Bosnia and Herzegovina and the FAFG lab in Guatemala are already helping Pro-Búsqueda in that regard.

What is the success rate?
For the last 18 years, Pro-Búsqueda has been the one organization in El Salvador searching for its disappeared children and has been successful in finding 382 children. But many more have yet to be found. We know of 539 additional confirmed missing children. But there is hope for the families, perhaps now more than ever. Times have changed. Though we are a mobile society, and that makes it difficult to find individuals so many years on, we also have technical approaches we can bring to the effort that make a difference. The DNA work is an active investigative tool as much as a confirming tool. So now, where we require the greatest ingenuity is in our outreach effort, to let the 500 or so young

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adults adopted from El Salvador during the conflict years know about Pro-Búsqueda and its efforts.

How are you sharing this work with others?
Using our second cycle of funding from the State Department, we are working on stimulating and supporting governmental agencies that need to become more versed in the technical aspects of missing persons investigations. As part of this, last May, Pro-Búsqueda and HRC sponsored a training event with the International Commission on Missing Persons (ICMP) in Sarajevo, sending an eight-person delegation from El Salvador to spend a week studying, witnessing, and learning the latest legal and scientific methods for finding missing persons. There is no one better than the ICMP if you want to see how it is done in a fully integrated fashion. The visit helped us illustrate what is possible and provide additional guidance to the El Salvadoran team.

Lack of recordkeeping, bureaucratic roadblocks, difficulty translating high science into effective legislation … these may seem like daunting challenges to newcomers. What advice do you have for others considering similar work in other regions?
It is a progressive effort that requires much cooperation. NGOs are often the first responders in times of war and conflict; they know what is happening before anyone else. So the question becomes, how do we mentor civil society organizations to collect forensic evidence adequately so that when it is brought to an appropriate court, international or national, it will be valid and useful? And this goes hand-in-hand with establishing, training, and following best practices. This is a critical part of the HRC's work with Pro-Búsqueda. We want to be sure that if Pro-Búsqueda were to present a kinship report in court, it will stand up very, very well. Things like demonstrating validated analysis conducted in fully accredited labs by proficiency-tested analysts, independent technical review of profiles, adequately written kinship reports, etc.

What does the future hold?
The next step, which will benefit the entire field, is more genetic markers. The more markers you can tie, the more information you can provide and the more certain you can be in your conclusions. This will allow us to resolve cases for which there is a paucity of close relatives to the child or young adult who was severed from his family. The other aspect where all ingenuity needs to be applied is finding the families who left El Salvador during the war, having already lost a child. I think the Internet and social media tools will make all the difference here.

This isn't your first foray into helping families of missing children. You were involved with the Grandmothers of Plaza de Mayo?
Yes. For me, this all began in 1984, during the military years in Argentina and Chile. So many thousands were

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missing, and grandmothers were looking for their grandchildren—the children of their missing or murdered children. Grandmothers of the Plaza de Mayo was the first organization I know of that reached out to the scientific community for assistance. They asked geneticists to help them find their grandchildren and make the connection to the grandparents, given the intervening generations were among the missing. This organization began to do its own investigations and realized science was required in order to confirm the relationships. I came to Washington in early 1984 and connected with the American Association for the Advancement of Science, which was requesting this kind of help under the leadership of Eric Stover at the AAAS (now faculty director at HRC) on the Grandmothers of Plaza de Mayo's behalf. I assisted in the organization of the scientific delegation that went to Argentina to support that work. The grandmothers have organized since and to this day impeccably. There you have the most advanced example of how an organization of families can learn science, use it, and have it work very well for the cause.

You presented on a panel exploring the connections between forensic professionals and human rights organizations. How do you feel these communities should interface with one another?

I think it is tremendously important that we discuss the growing connection between the forensic and human rights communities. As forensic scientists and organizations, I believe we have an obligation to the civil society organizations of the world, addressing how investigations can be initiated and sustained in the absence of other institutions coming to their service. We know states tend to be resistant to investigating their own deeds, in any form, particularly crimes of war and genocide. This poses difficult challenges for organizations seeking the truth. We must reach out to these organizations and train them to use science and technology intelligently. In the meantime, we will be transformed and see much more clearly, I think, why and how we should invest in science.

For further reading and links, go to www.forensicmag.com/article/their-dna-finding-el-salvadors-missing-children.

President of Barten & Associates consulting and a longtime freelance writer, **Laura Barten** *has written about health care, science, marketing, finance, work life, travel, and the arts since 1990. Barten holds a BA in journalism and political science and an MBA in marketing from the University of Wisconsin-Madison. www.linkedin.com/in/laurabarten*

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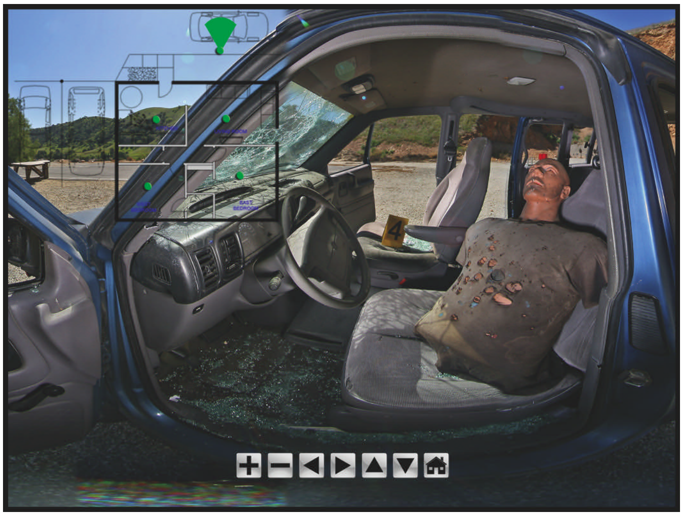

Image 1: This mock virtual tour allows investigators using a desktop computer or a mobile device to take a self-guided room-to-room visual tour of the entire crime scene. Investigators can navigate from one location to another simply by clicking on the green "hotspot" from the map (upper left). The sweeping radar icon indicates the current direction of the rotating panorama.

Crime Scene 360

In addition to your typical crime scene photography, it is not too difficult to capture the panoramic images necessary to create a virtual tour of the scene.

Tony Nguyen

Whether you are a cold case detective revising an old case or a forensic investigator presenting in court, wouldn't it be great to be able to revisit the crime scene again as if you were actually there? Now you can! With today's exciting technology, it is possible to actually experience being at the crime scene via a "virtual tour" allowing you to view it in any direction (Image 1). In addition to normal crime scene photography, it is not too difficult to capture the panoramic images you need to create this virtual tour…all you'll need after that is simple hardware and software.

There are two types of panoramas that are useful to the forensic community:

- Spherical Panorama which captures a 360° field of view in all directions around the photographer.
- Object VR (Virtual Reality) which allows a photographed object to be rotated in all directions.

This article will focus on spherical panoramas. There are multiple ways of creating spherical panoramas, and the following process is based on hardware and software that I am currently using. It is by no means the only method of producing these panoramas.

Part One: Hardware

Only five pieces of hardware are needed to create a panoramic image:

1. Digital SLR camera – Use the same camera you have in your crime scene kit since you are familiar with its functions.
2. 8mm fisheye lens
3. Panoramic head
4. Tripod
5. Shutter release

Why 8mm?

Any lens will work; however, you will need to capture more images to complete a sphere with a longer focal length than a wide angle lens. For example, an 8mm fisheye lens will capture the entire 360° sphere with just four images in a single row versus a 16mm lens that requires six or more images in two rows (Images 2 and 3). The fewer the number of images, the fewer stitches that need to be prepared… which means less computer processing time.

The 8mm fisheye lens also accentuates nearby objects by enlarging them; and minimizes those that are at a distance by making them smaller. The objects, therefore, seem farther apart than they really are, creating an elongated perspective helping to reduce the parallax effects (discussed in the next section). For this reason, utilizing a panoramic head is not always necessary if there is no foreground object within two meters of the camera lens. Hence, the fastest and easiest way to create spherical panoramas is with the widest lens available—the 8mm fisheye. However, the techniques outlined here will result in an opti-

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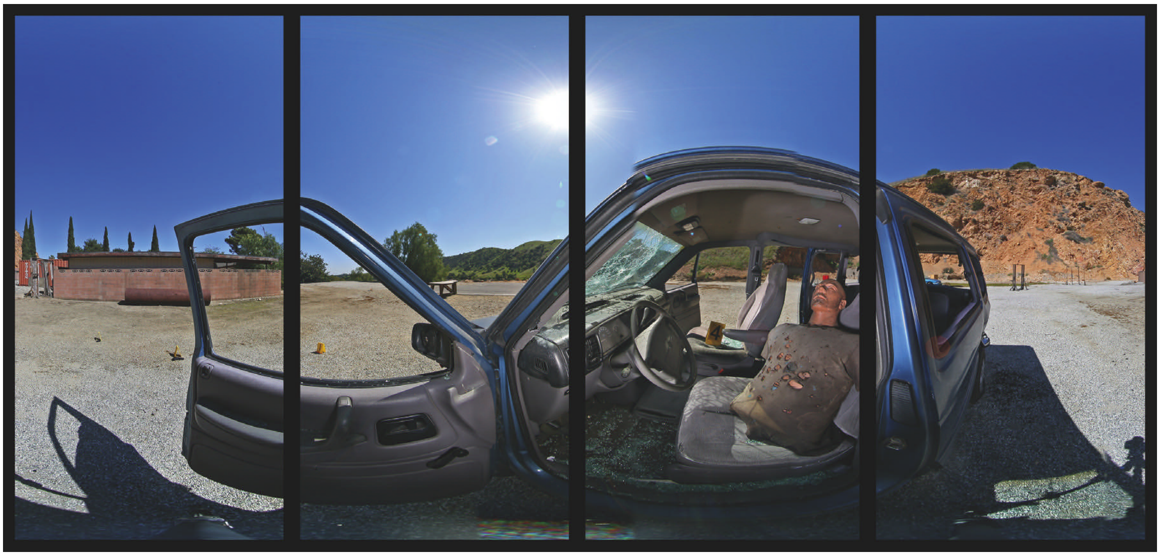

Image 2: Four overlapping images captured with an 8mm fisheye lens in a single row.

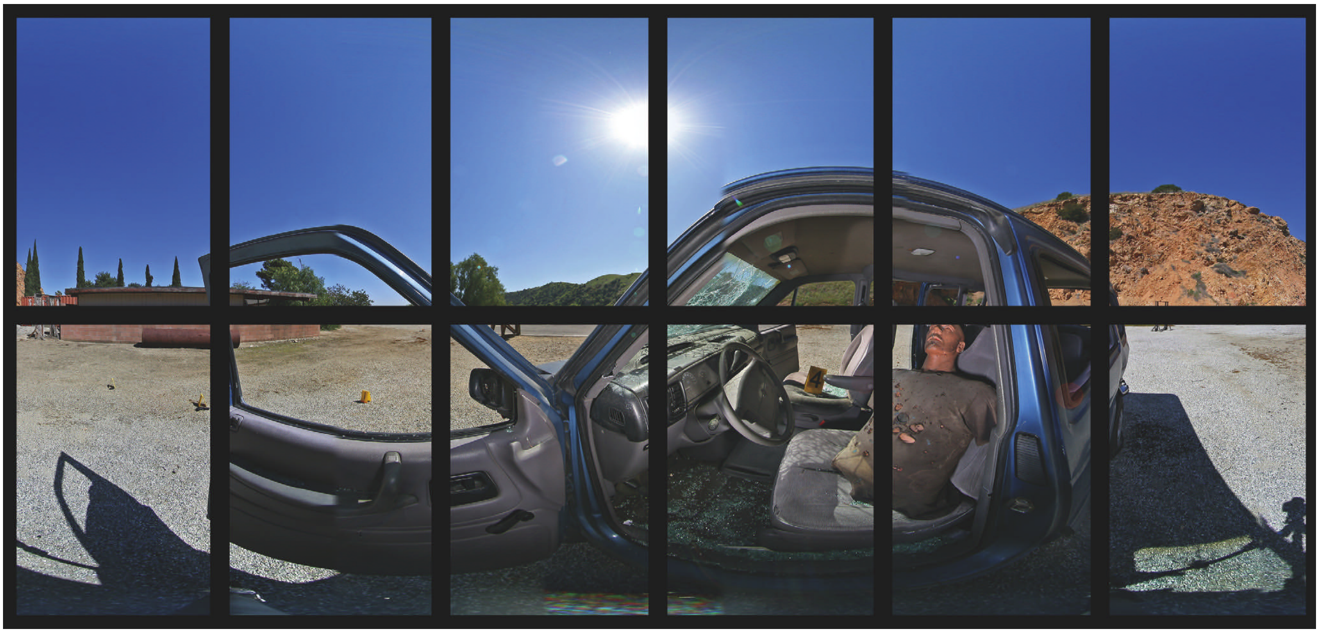

Image 3: Twelve overlapping images captured with an 16mm lens in two rows.

mal panorama, regardless of lens choice.

Panoramic Heads

Parallax is the movement of a foreground object in relation to the background which causes some degree of misalignment between two adjacent photographs during the stitching process (Image 4). Parallax errors occur when photographs are captured by rotating the base of the camera on a standard tripod instead of rotating the lens.

To experience the effect of parallax just hold your thumb out at arm's length and align your thumb with an object in the distance. Then, close one eye and without moving your thumb, rotate your head left to right—your thumb will move to the left or right side of the distant object while

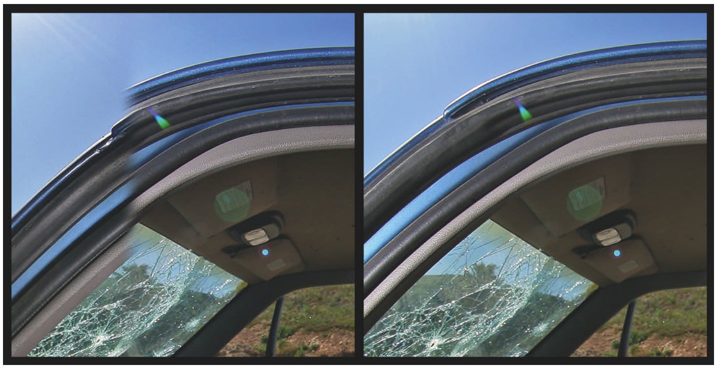

Image 4: Misalignment during stitching causes a parallax error (left) which can be corrected by using a panoramic head during the image acquisition (right).

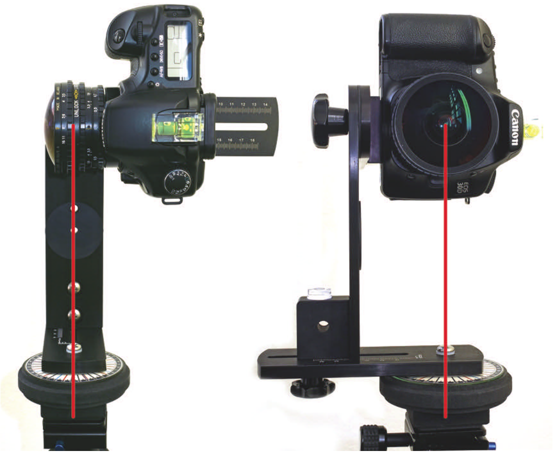

Image 5: Aligning the optical center of the lens directly over the axis of rotation of the panoramic head.

Image 6: 8mm image captured from an APS sized DSLR.

the background remains stationary—this is parallax. Essentially your eye is the camera lens and your neck is the tripod.

To completely eliminate parallax errors, the camera needs to rotate about the entrance pupil (nodal point) of the lens which is generally around the front barrel of the lens. Panoramic heads are designed to position the nodal point of the lens over the center of the rotation of the tripod (Image 5). There is a wealth of information on Web sites that dedicate themselves to the collection of entrance pupil locations for a miriad of different lenses. Just search for your particular lens. Here is one source: //wiki.panotools.org/Entrance_Pupil_Database.

There are numerous different styles of panoramic heads available. They range from the affordable, Panosaurus; the most popular, Ninja Nodal; and even robotic automation heads, Gigapan. My preference will always be based on size and weight. Of course, budget does come into play. The smallest, lightest, and easiest pieces of hardware to use are the ring clamp style of panoramic head. I leave the ring mounted on the fisheye full-time in storage, therefore no setup time is wasted when it's time to use it.

Part Two: Image Acquisition

I will assume that you have some working knowledge of basic photography and an understanding of your camera functions.

The basic idea here is to capture all 360° of the scene by overlapping multiple photographs, roughly 20–30% with each adjacent photograph. Keep in mind that there are certain key requirements unique to panorama photography that must be adhered to in order to create a seamless panorama.

Camera Settings

Each of the photographs taken must use an identical setting since any inconsistency in exposure, focus, or white balance between shots will create a mismatch during the stitching process. The same holds true for the lens' focal length if a zoom lens is in use; tape down the lens barrel if necessary.

- Ensure the resolution is at the largest setting and ISO at the lowest to get the best quality and cleanest images.
- Lock your white balance according to the current environment lighting condition (unless you are shooting RAW files).
- Set the camera to full manual mode "M" and the shutter speed as required for correct exposure.
- Set the aperture to your lens' "sweet spot," usually somewhere in the mid-range apertures of f/8 to f/11 to produce the sharpest images. Setting it to f/22 or higher may yield more depth-of-field but will degrade image sharpness.
- Manually lock focus on the main subject or use the hyperfocusing method for best results. Since the fisheye lens captures images at such an extreme angle, it has a very large apparent depth of field. This means that the photograph will appear sharply focused from front to back even at a wide aperture.
- Avoid using on-camera flash. Use a slower shutter speed or off camera lighting that can stay consistent throughout the rotation of the camera.

Landscape or Portrait Mode

With a full-framed sensor camera, the fisheye lens will capture a full 180° view in all directions and produces a complete circular image at the center of the frame surrounded by black unexposed areas on the outer edges of the frame; therefore, the camera can be used in either orientation. However, landscape mode will probably be more stable.

With the 8mm fisheye on an APS cropped sensor, the camera produces an image with 180° coverage along the widest length of the frame. However, the sides are cropped out creating an incomplete circle. It is best to use the camera in the portrait orientation for the top and the ground coverage. And due to the cropped sides, additional images need to be taken to create a complete 360° around the horizontal rotation (Image 6).

Part Three: Software

Now that the scene images are captured, the next step is to assemble them using specialized software that is capable of creating spherical panoramas.

Depending on the end results of the panoramic project, whether you want to create a standalone scene or a virtual tour of multiple scenes, two types of software will be needed:

1. Stitching software
2. Touring software

Stitching software will seamlessly stitch, blend, and then export images as a single scene. They also have additional features such as RAW import, viewpoint corrections, and High Dynamic Range (HDR) panorama creation. Three of the most used stitching software products are PTGui Pro, Panoweaver, and Autopano Pro.

Touring software organizes multiple scenes into an interactive virtual tour. The viewer is then able to navigate the scene and access it from one location to another via mouse drag, buttons, and mapping. The basic elements for all touring software are the clickable "hotspot" creation. The hotspot can be programmed to open another scene, display a photo, open an external file such as a video, or to display contextual information in a popup window. The software also supports the final virtual tour output in readily available non-proprietary software formats such as Adobe Flash or HTML5 for playback.

There are many software choices and it is recommended that you download a free trial version, give it a try, and see which vendor has the work flow that fits your needs.

Last Shot

There will always be a learning curve when acquiring new skills, so don't get frustrated or discouraged. It is merely a matter of perfecting and building on what is learned at each step and it will get easier.

One final tip, take a photograph with the lens cap on in between each panoramic scene. This will visually separate out the scenes during the stitching process.

Tony Nguyen *is a Crime Scene Investigator and a Latent Print Examiner with the Pomona Police Department in Southern California. He currently serves as a board member on the IAI Forensic Photography & Imaging Certification Board and as a 2nd Vice President for the Southern California Association of Fingerprint Officers (SCAFO). He has a degree in Commercial Photography from the Art Institute of Seattle in 1989, has been a professional photographer since 1990, and has had photography exhibitions throughout California, Washington, Vancouver (BC), and Victoria (BC).*

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The Future of Forensics Has Arrived: The Application of Next Generation Sequencing

Walther Parson, Ph.D.; Sharon Wootton, Ph.D.; and Lisa Lane Schade, MHR

Over the last two decades, numerous innovative technological advances have fueled the expansion of the biological and chemical sciences. Following refinement and rigorous testing, many have been adopted by forensic DNA testing laboratories, including polymerase chain reaction, capillary electrophoretic instrumentation, automated liquid handling, and expert software systems. Robust validation processes often slow the introduction of new tools available to test evidentiary samples. However, this methodical diligence has protected the credibility of DNA and resulted in DNA becoming the gold standard for forensics and the most effective crime fighting tool available to law enforcement.[1]

The progression from Sanger-type sequencing (STS) to next generation sequencing (NGS) will further advance the regenerative sciences, personalized medicine, and forensics. Today, mitochondrial sequencing (mtDNA) is already a validated, widely accepted and utilized tool for helping to resolve complex cases. Advances in this method, through the introduction of next generation systems, are only one way in which these new discoveries will provide additive information to forensic cases.

Laboratories are expected to migrate from today's current methods including mitochondrial sequencing, to more efficient technology platforms. In addition, forensic facilities that offer specialized testing for missing persons and mass disaster victim identification will gain great capabilities leveraging these next generation testing systems.

What is it?

Next-generation sequencing

The emergence of NGS technologies has yielded an unprecedented wealth of data, enabling advancement of genomic practices including whole genome sequencing, RNA-seq, and massively parallel single nucleotide polymorphism (SNP) and amplicon resequencing. A number of smaller-scale bench top NGS platforms have surfaced to accommodate the needs for an affordable, fast, easy-to-use instrument.[2] These platforms deliver from 10 mega-bases to several giga-bases of sequence in a matter of hours to days and allow for multiplexing across both sample and loci.[3] With this level of throughput, forensic applications can now be approached with NGS.

How can it be used?

NGS Applications in Human Identification

Among the breadth of utilities, the most common ones utilized for forensic testing include sequencing of STRs, SNPs, and mtDNA. First, NGS technology enables large multiplexes with comparable or greater than existing power of identities of commercial kits to be sequenced. In addition to providing discriminatory power based on length of allele, NGS yields sequence content, which can then be used to further dissect mixtures by base composition in the highly polymorphic repeat structure. Second, in the presence of scant or degraded DNA, identity or kinship analysis can be conducted with fragments as short as 60–70 nucleotides. Other SNP classes, including ancestry-informative SNPs, could be employed in the future to assist in routine forensic analysis and provide investigative leads and subject exclusion.[4] Third, haplotyping for kinship, phylogenetics, or analysis of degraded DNA can be carried out by sequencing Y-SNPs or mtDNA. With the latter, either the mitochondrial genome can be sequenced in its entirety or only a portion such as the highly polymorphic sites and regions including the D-loop. Finally, it is possible that all of these applications can be completed in parallel because multiplexes can be designed in any combination preserving sample while speeding up the availability of probative information available to law enforcement for use in active cases.

How does it work?

Workflow from Sample to Data

In general, NGS involves three fundamental parts—library prep, sequencing, and data analysis (Figure 1). Whether working from genomic DNA or total nucleic acid of a metagenomic sample, library preparation involves obtaining fragments or amplicons of DNA of appropriate sequencing length (200bp to 400bp) and flanking them with adaptors to be used in template preparation and sequencing (Figure 1b). Prior to sequencing, most platforms require a step to clonally amplify templates with the correct adaptor topology—bead-based emulsion PCR (Figure 1c). This product serves as a template for each sequencing reaction. In semiconductor-based sequencing, incorporations of natural nucleotides are interpreted by transistors sensitive to the release of hydrogen ions during polymerization[5] (Figure 1d). These signals are then translated into sequence, and the resulting data files are used as the input to bioinformatics pipelines that deliver a variety of results, from genotype to a consensus of a genome.

Does it work?

One Example: Sequencing of mtGenomes with the PGM

Highly compromised samples often cannot be successfully characterized with autosomal DNA markers, even employing next generation STR chemistry. The analysis of mtDNA has become the last resort of hope for such samples, because it is present in much higher copy numbers in the cell and therefore is more likely to provide useful results. The major limitation of its application to forensics has been the relatively low discrimination power of mtDNA as maternally related individuals share the same haplotype. Historically the so-called hypervariable segment 1 (HVS-1) of the mitochondrial control region, the only larger non-coding region in the mtGenome, was targeted, providing a random match probability (RMP) of roughly 1 in 30 individuals. With the entire mtDNA control region the RMP augmented to 1 in 120 and has provided useful evidence in many cases.[6] The extension to analyze the entire mtGenome is a logical consequence and desirable goal to maximize the information content of mtDNA analyses.[7] Conventional Sanger-type sequencing may however not be the suitable method as it is laborious and prone to error, as previous studies have shown.[8] In the early years of mtDNA typing antecedent versions of the sequencing polymerase resulted in numerous phantom mutations[9] but more frequently were transcription error[10] and artificial recombination[11] responsible for flawed data. In an effort to increase the quality of forensic mtDNA databasing the EMPOP project (www.empop.org),[12] offered new protocols for mtDNA typing, revised guidelines for reporting mtDNA evidence[6] and introduced a novel mtDNA database query engine for the retrieval of reliable frequency estimate.[13] Meanwhile, the two leading forensic genetic journals *Forensic Science International Genetics* and *International Journal of Legal Medicine* require authors to have mtDNA population studies quality controlled by EMPOP prior to submission for review, which significantly improved the overall quality of published mtDNA population data in forensic genetics since 2010.

Early problematic NGS data on mtGenomes show that a posteriori quality control is becoming increasingly necessary with the move to parallel sequencing technologies.[14] In order to evaluate the performance and reliability of current NGS, a comparative study on 64 mtGenomes from diverse phylogenetic backgrounds (sub Saharan African, Southeast Asian, and West Eurasian) and different biological sources (blood, buccal swabs, and paraffin-embedded tissue) was performed using the PGM and STS as reference method.[15] Twenty-two of those mtGenomes were sequenced redundantly using two different sequencing chemistry versions (100 bp and 200 bp chemistries) on the PGM to investigate the effect of different reading lengths on the sequencing precision (Figure 2).

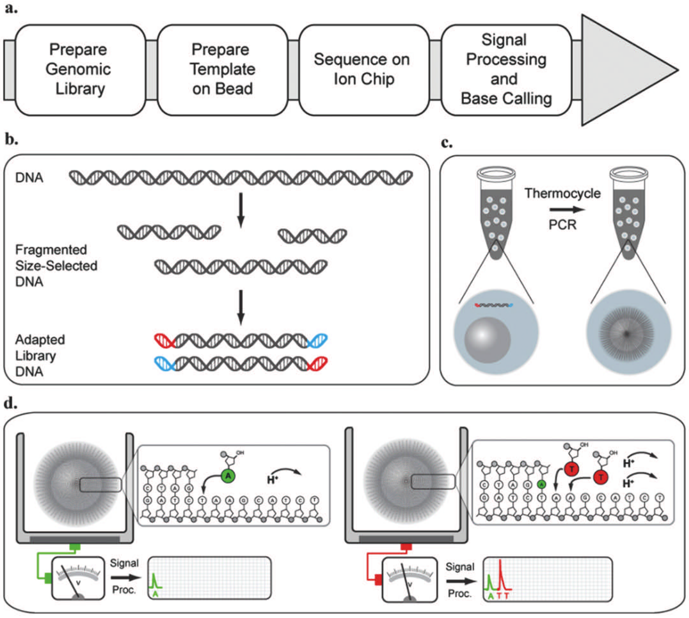


Figure 1: Semiconductor based next generation sequencing.

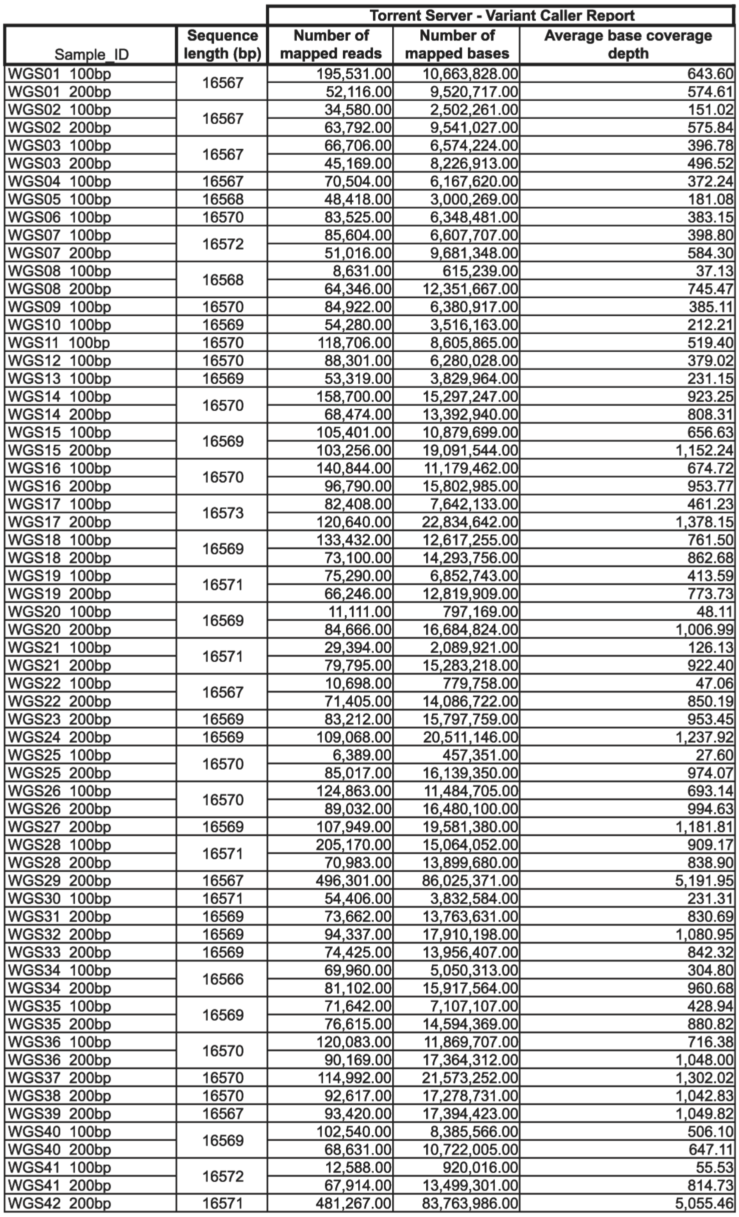
The DNA library was set up by long range PCR amplification of two 8.5 kbp fragments and enzymatically sheared to yield the required fragment sizes of 130 and 260 bp. Adaptors were ligated and amplicons enriched using the Ion Torrent chemistries and instrumentation (Ion One Touch) and the targets subsequently sequenced on a 316 chip. The 64 mtGenomes encompassed a total of 1,060,437 bp (Figure 2) that were directly compared between the two technologies.

In total, our laboratory identified 176 differences between outputs from STS (consensus sequences from redundant reactions) and the Ion Torrent mito variant caller (applying a threshold of 20% variant call frequency of total coverage). This equals a difference rate of 0.017%. The majority of differences (n=108, 61.4%) were found to lie within or in the vicinity of homopolymeric sequence stretches and the application of different alignment algorithms (paired read) provided evidence that those differences did not concern physical PGM generated data but largely depended on the applied alignment method. These results are extremely promising and are expected to significantly increase the RMP for mtDNA analysis when evaluating highly compromised samples.

What's Next?

NGS is one of the most relevant advances that continue to revolutionize the sciences and fuel discovery. Forensic DNA testing is no exception. By applying the most sophisticated technology and through relentless validation and testing of the latest technologies, forensic analysts have access to tools that provide the most informative results. And, obtaining the best and most probative results is important when evaluating criminal cases. While the application of NGS to mtDNA sequencing is occurring today, it is anticipated that new panels will be developed and utilized to produce results in highly complex cases, including missing persons and mass disaster victim identification in the very near future. And as specialty centers begin implementing these for use in forensic investigations, they will also pave the way for analysts to further leverage the power of next generation sequencing for routine forensic investigative purposes.

View references at www.forensicmag.com/article/future-forensics-has-arrived-application-next-generation-sequencing.



		Torrent Server - Variant Caller Report		
Sample_ID	Sequence length (bp)	Number of mapped reads	Number of mapped bases	Average base coverage depth
WGS01 100bp	16567	195,531.00	10,663,828.00	643.60
WGS01 200bp		52,116.00	9,520,717.00	574.61
WGS02 100bp	16567	34,580.00	2,502,261.00	151.02
WGS02 200bp		63,792.00	9,541,027.00	575.84
WGS03 100bp	16567	66,706.00	6,574,224.00	396.78
WGS03 200bp		45,169.00	8,226,913.00	496.52
WGS04 100bp	16567	70,504.00	6,167,620.00	372.24
WGS05 100bp	16568	48,418.00	3,000,269.00	181.08
WGS06 100bp	16570	83,525.00	6,348,481.00	383.15
WGS07 100bp	16572	85,604.00	6,607,707.00	398.80
WGS07 200bp		51,016.00	9,681,348.00	584.30
WGS08 100bp	16568	8,631.00	615,239.00	37.13
WGS08 200bp		64,346.00	12,351,667.00	745.47
WGS09 100bp	16570	84,922.00	6,380,917.00	385.11
WGS10 100bp	16569	54,280.00	3,516,163.00	212.21
WGS11 100bp	16570	118,706.00	8,605,865.00	519.40
WGS12 100bp	16570	88,301.00	6,280,028.00	379.02
WGS13 100bp	16569	53,319.00	3,829,964.00	231.15
WGS14 100bp	16570	158,700.00	15,297,247.00	923.25
WGS14 200bp		68,474.00	13,392,940.00	808.31
WGS15 100bp	16569	105,401.00	10,879,699.00	656.63
WGS15 200bp		103,256.00	19,091,544.00	1,152.24
WGS16 100bp	16570	140,844.00	11,179,462.00	674.72
WGS16 200bp		96,790.00	15,802,985.00	953.77
WGS17 100bp	16573	82,408.00	7,642,133.00	461.23
WGS17 200bp		120,640.00	22,834,642.00	1,378.15
WGS18 100bp	16569	133,432.00	12,617,255.00	761.50
WGS18 200bp		73,100.00	14,293,756.00	862.68
WGS19 100bp	16571	75,290.00	6,852,743.00	413.59
WGS19 200bp		66,246.00	12,819,909.00	773.73
WGS20 100bp	16569	11,111.00	797,169.00	48.11
WGS20 200bp		84,666.00	16,684,824.00	1,006.99
WGS21 100bp	16571	29,394.00	2,089,921.00	126.13
WGS21 200bp		79,795.00	15,283,218.00	922.40
WGS22 100bp	16567	10,698.00	779,758.00	47.06
WGS22 200bp		71,405.00	14,086,722.00	850.19
WGS23 200bp	16569	83,212.00	15,797,759.00	953.45
WGS24 200bp	16569	109,068.00	20,511,146.00	1,237.92
WGS25 100bp	16570	6,389.00	457,351.00	27.60
WGS25 200bp		85,017.00	16,139,350.00	974.07
WGS26 100bp	16570	124,863.00	11,484,705.00	693.14
WGS26 200bp		89,032.00	16,480,100.00	994.63
WGS27 200bp	16569	107,949.00	19,581,380.00	1,181.81
WGS28 100bp	16571	205,170.00	15,064,052.00	909.17
WGS28 200bp		70,983.00	13,899,680.00	838.90
WGS29 200bp	16567	496,301.00	86,025,371.00	5,191.95
WGS30 100bp	16571	54,406.00	3,832,584.00	231.31
WGS31 200bp	16569	73,662.00	13,763,631.00	830.69
WGS32 200bp	16569	94,337.00	17,910,198.00	1,080.95
WGS33 200bp	16569	74,425.00	13,956,407.00	842.32
WGS34 100bp	16566	69,960.00	5,050,313.00	304.80
WGS34 200bp		81,102.00	15,917,564.00	960.68
WGS35 100bp	16569	71,642.00	7,107,107.00	428.94
WGS35 200bp		76,615.00	14,594,369.00	880.82
WGS36 100bp	16570	120,083.00	11,869,707.00	716.38
WGS36 200bp		90,169.00	17,364,312.00	1,048.00
WGS37 200bp	16570	114,992.00	21,573,252.00	1,302.02
WGS38 200bp	16570	92,617.00	17,278,731.00	1,042.83
WGS39 200bp	16567	93,420.00	17,394,423.00	1,049.82
WGS40 100bp	16569	102,540.00	8,385,566.00	506.10
WGS40 200bp		68,631.00	10,722,005.00	647.11
WGS41 100bp	16572	12,588.00	920,016.00	55.53
WGS41 200bp		67,914.00	13,499,301.00	814.73
WGS42 200bp	16571	481,267.00	83,763,986.00	5,055.46

Figure 2

Lisa Lane Schade *is the Director of Global Market Development for the Human Identification Business at Life Technologies. For over a decade, she's worked with forensic scientists and thought leaders throughout the world to develop programs and products targeted at solving complex forensic challenges.*

Sharon Wootton *received her Ph.D. in Bioengineering from UC Berkeley. She is a senior research scientist working on next generation forensic technologies at Life Technologies.*

Walther Parson *leads an active group of scientists that published more than 200 peer-reviewed articles in the forensic and medical genetic field within the past 10 years at the Institute of Legal Medicine in Innsbruck Medical University. His research helped to establish the National DNA Database Laboratory of the Austrian Federal Ministry of the Interior, and he is an expert in using advanced DNA techniques to resolve highly complex identification cases.*

Touch DNA: From the Crime Scene to the Crime Laboratory

While touch DNA has become a much requested and successful test for DNA laboratories to perform, we must remember its limitations and be aware of the factors which may affect the results.

Joe Minor

When Edmond Locard proposed his Exchange Principle, he could not have imagined the implication it would have on forensic science today. Indeed, in the field of DNA testing, does "Every contact leave a trace" as Locard stated?

Initially in forensic serology, the "trace" left behind was a bloodstain containing antigens and polymorphic enzymes. Blood was visible in most cases for testing, but the end result was not always very discriminating. When Restriction Fragment Length Polymorphism (RFLP) DNA profiling was developed in the early 1990s, forensic serologists were excited to be part of a new generation of testing which was now being conducted at the molecular level. This early DNA testing required a relatively large amount of DNA for the development of a DNA profile, and the bloodstain left behind was still visible or detectable using presumptive tests.

By the late 1990s RFLP testing was being replaced by the Polymerase Chain Reaction (PCR) based short tandem repeat (STR) DNA typing method. A new era of trace DNA detection had begun. The quantity of DNA required for analysis had been dramatically reduced. What was once a visible bloodstain had now become a speck of blood barely visible to the naked eye. As STR testing continued into the new millennium, DNA profiles were beginning to be developed from evidence where there was seemingly no bloodstain or other body fluid present. This trace or "touch" DNA, as it is now referred to, led to many questions. What had changed? How can we test evidence for skin cells? Will the results be meaningful or probative to the case? How do we process a crime scene and collect evidence? How do we address contamination? Is touch DNA really a different technology?

Touch DNA

Epithelial or touch DNA evidence can be defined as evidence with no visible staining that would likely contain DNA resulting from the transfer of epithelial cells from the skin to an object. Can simply touching an object leave skin cells? It has been stated in publications that forensic scientists can obtain a DNA profile from as few as five to six cells. However, just because a surface is touched and a few skin cells are left behind does not guarantee a meaningful DNA profile can be obtained. Detecting and obtaining an interpretable DNA profile are two different concepts.

The touch DNA testing performed by most public crime laboratories utilizes the same STR typing method performed by DNA analysts for the last 10–15 years. It is not a new technology. There are alternate methods of detecting DNA from a smaller number of cells ranging from 15–30 diploid cells. This is known as Low Copy Number (LCN) testing and utilizes "enhanced" techniques for obtaining DNA profiles. The experts and courts have had disagreements on its validation, interpretation, use, and acceptance. Typically, STR typing is known to require approximately 70–150 cells to produce a DNA profile.

Why are DNA labs receiving more touch DNA requests?

Crime laboratories are receiving more property crime cases than ever before. The Combined DNA Index System (CODIS) has produced a large percentage of hits obtained from property crime cases and these profiles have been connected to other types of offenses as well. Violent crime cases with no blood or semen are being submitted to DNA labs in the hope that touch DNA testing may provide investigative leads. Cold cases where there may not have been body fluids left behind or the samples were too degraded are now being resubmitted to DNA labs.

Why are labs seeing more success with touch DNA cases?

Evidence collectors have more training in recognizing suitable items potentially handled by a suspect and how to collect touch evidence. DNA typing kits have improved in sensitivity and the number of loci detected, and instrumentation has improved in the areas of extraction, quantitation, and instrumental analysis.

What makes it likely that a suspect may leave his touch DNA on an item?

Some suspects are known to shed cells more than others. It is known that we shed approximately 400,000 cells daily.[1] Does this mean suspects are like the *Peanuts* character, Pigpen, walking around leaving a cloud of cells capable of producing several thousand DNA profiles? The clothing worn by suspects reduces the number of cells that can slough off and deposit themselves on a surface capable of producing DNA results. Suspects are nervous and tend to perspire more during the crime, leaving more cells behind. A suspect may touch his face or head and transfer a large number of cells to his hands or gloves. Also, the rougher the surface texture, the higher the probability of abrading skin cells. Stronger contact pressure applied to the item also increases that probability.

Processing the Touch DNA Crime Scene

Is the crime scene technician wearing the appropriate personal protective equipment (PPE)? I sometimes refer to the image of a television crime scene investigator and ask my students, "What is wrong with this picture?" The image shows the investigator wearing latex gloves, but no hat, no mask, a short sleeved shirt, and dusting an item for prints. Epithelial cells from the head, arms, mouth, and nose may be left on crime scene evidence by the investigator. As far as dusting for prints is concerned, are the brush and powder disposable so as not to transfer cells from other items or even a previous crime scene?

Contamination is the unintentional introduction of outside DNA into a crime scene or laboratory sample. Contaminant DNA may appear as background DNA, the major or minor profile within a mixture, a single source DNA profile, or all of the above. When can this occur? Before the commission of the crime, after the crime and before the crime scene is discovered/secured, during the crime scene investigation, and within the crime laboratory or DNA laboratory (Figure 1).

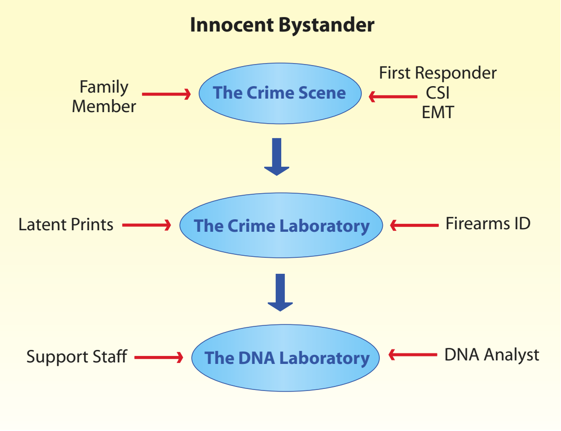


Figure 1: Potential Sources of Epithelial Contamination

Common rules to help minimize contamination at the crime scene:

- Limit access to the crime scene or evidence
- Do not talk over the evidence
- PPE, including masks
- Change gloves frequently after handling evidence
- Do not touch areas on evidence that may be sampled for DNA
- Collect elimination samples from those who have been in contact with the evidence or scene
- Use disposable fingerprint brushes and powder
- Clean each crime scene tool coming into contact with evidence

Communication with the laboratory

A detailed request/submission form is necessary to alert laboratory personnel prior to analysis that potential touch DNA evidence may be present.

Indicate if the suspect is a stranger or has been in contact with the scene. Note on the request if any of the touch exhibits will be shared with another section of the laboratory. This alerts other sections to take the appropriate measures to protect the touch DNA evidence. Provide the appropriate elimination standards whether from law enforcement, crime scene personnel, or individuals known to be in contact with the victim or scene. Follow up a touch DNA request with a phone call. Crime scene investigators should check with their forensic laboratory as it may have an evidence policy specifically for touch DNA evidence acceptance and examination.

The DNA Lab and Contamination

Once evidence is received into the DNA laboratory, how is contamination minimized and what are the potential sources of epithelial cells? The *Quality Assurance Standards for Forensic DNA Testing Laboratories* addresses DNA contamination in Standard 9.7. In the discussion section it states, "A laboratory shall have and follow a documented policy for detecting and controlling contamination. This policy should include the procedures used by a laboratory *for monitoring, decontaminating, and detecting contamination*. In addition, a laboratory shall have and follow policies and/or procedures for interpreting data potentially affected by contamination."[2]

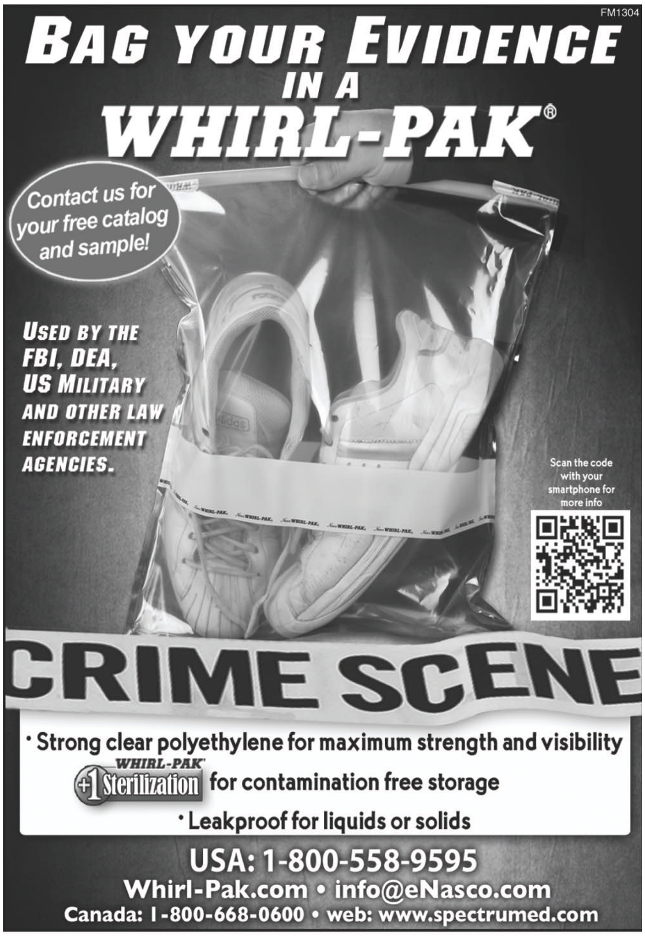
In addition to lab coats and masks, how is contamination detected, controlled, and monitored? Some examples which may be employed are:

- Access to the laboratory shall be controlled and limited to prevent access by unauthorized personnel.
- Separation of the work areas for evidence examination, DNA extraction, and DNA amplification and typing.
- Exhibits are examined at different locations and/or times.
- Negative controls are being used from evidence examination through extraction and amplification.
- Contamination logs monitor introduction of exogenous DNA and identify sources.
- Elimination profiles of past and present DNA analysts or support staff are maintained.

The European Network of Forensic Science Institutes (ENFSI), the FBI Laboratory's Scientific Working Group on DNA Analysis Methods (SWGDAM) composed of U.S. and Canadian members, and the Australian Biology Specialist Advisory Group (BSAG) published a joint position statement advocating that forensic DNA laboratories maintain an elimination database for screening DNA results as appropriate.[3]

Contamination Events

In some recent cases both in the U.S. and the UK, there have been DNA profiles developed from crime scene evidence where the profiles matched a crime scene technician or DNA analyst and the information had been erroneously reported as a possible suspect profile. This can be avoided as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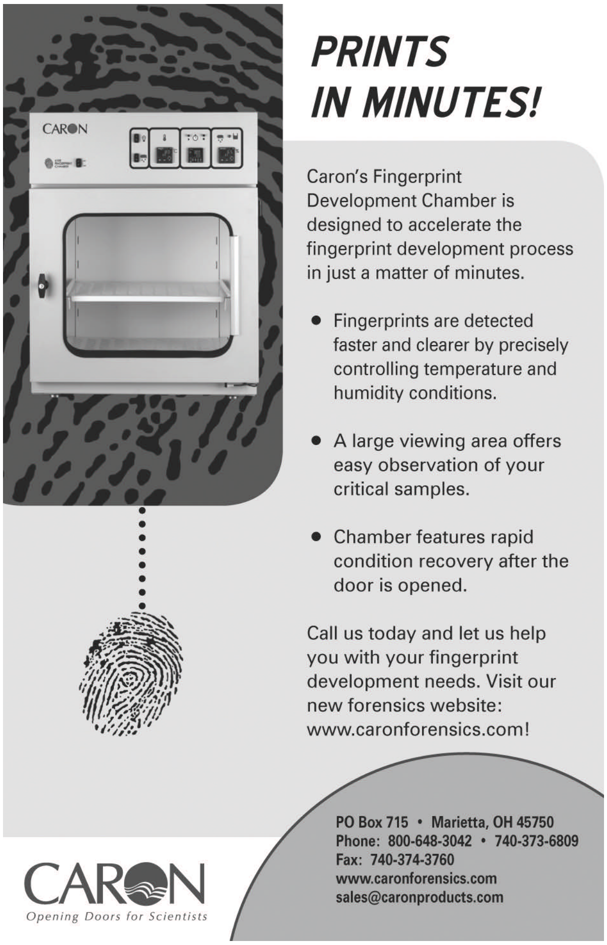
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long as we have the relevant DNA elimination databases. In one particular example, staff profiles from DNA analysts were not being maintained. An unknown profile was obtained and given to detectives as an investigative lead. It was later discovered the profile belonged to a DNA analyst. In a recent request for a new trial based on skin cells found on evidence not matching the defendant's DNA, the Maine Judicial Supreme court ruled that there were other plausible sources for the male DNA, including detectives at the crime scene and forensic investigators who later handled the evidence. Later analysis of the DNA showed that the traces of male DNA could have come from a fingerprint brush the latent print analyst had used in other cases.[4]

What are some of the problems encountered with touch DNA cases?

- No presumptive tests
- Partial profiles yielding low statistics
- Complex Mixtures: A mixed sample may contain background DNA, crime-related DNA, and post-crime contamination, and it may be difficult to identify the relevant profile.
- Increased chance of contamination
- The profile may not be sufficient to enter into CODIS
- A late touch DNA request for examination of shared evidence
- Re-examination of cold cases which may not have been collected, stored, or examined with trace DNA detection sensitivities in mind.
- Touch DNA does not tell you "when" or "how" DNA was deposited
- Background DNA obtained from clothing which was handled by someone else or by the manufacturer
- A bloodstain containing epithelial cells from another source

Successful Touch DNA Results

I have seen touch DNA results obtained from some unusual sources. These included DNA profiles developed from a pocket lining, grips from weapons, asphalt, face epithelials transferred to clothing, utensils, shoestrings, and a victim's oral swab which contained DNA from the suspect's tongue. On one occasion, I swabbed my own hand after handshakes at a social function to determine the presence of other epithelial cells. The laboratory was able to obtain a mixture of my DNA as well as two other individuals.

While touch DNA has become a much requested and successful test for DNA laboratories to perform, we must remember its limitations and be aware of the factors which may affect the results. These include:

- Was the amount of DNA adequate for meaningful interpretation?
- Was contamination minimized and accounted for?
- Did uninvolved individuals have access to the scene or victim?
- Was it likely that a suspect could have deposited epithelial cells on the surface of the evidence?

If every contact leaves a trace, as Locard stated, then we must be prepared to answer these questions.

View references at www.forensicmag.com/article/touch-dna-crime-scene-crime-laboratory.

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John J. Barbara

Mozilla Firefox Forensics: Part 4

Firefox Database Files

Each User on a system has his or her own SQLite RDMS in their profile and it is important to note that the data in the files is profile specific. Firefox (version 16.0.2) typically includes twelve SQLite databases, each of which performs a different function such as to store bookmarks, cookies, places visited, searches, and so forth. All date/time stamps in the tables are stored as UNIX numeric values which can be decoded by using an application such as "DCode."

places.sqlite

The file contains a list of all Web sites visited, bookmarks, and attributes for those sites. Forensically, it is probably the most important file for investigators to examine. A User's entire Web history, including all bookmarks, their properties, and favorite icons are maintained in the file. This information can be linked to the cookies.sqlite, formhistory.sqlite, and permissions.sqlite files to provide an overall view of a User's Internet activity. The file contains thirteen tables:

- moz_anno_attributes
- moz_annos
- moz_bookmarks
- moz_bookmarks_roots
- moz_favicons
- moz_historyvisits
- moz_hosts
- moz_inputhistory
- moz_items_annos
- moz_keywords
- moz_places
- sqlite_sequence
- sqlite_stat1

All bookmarks are stored in the "moz_bookmarks" table. The "title" column contains the name of the bookmark and the "dateAdded" column contains the timestamp information. Bookmarks can be linked to the URLs in the "moz_places" table since the "fk" column in "moz_bookmarks" contains the same values as those in the "id" column in the "moz_places" table.

Each time a User visits a Web page, an entry is recorded in the "moz_historyvisits" table. The date of the visit is recorded in the "history_date" column and how the User arrived at the site is recorded in the "visit_type" column. Values in this column can be very important forensically:

- "1" the User followed a link.
- "2" the User typed/allowed the autocomplete feature to complete the URL.
- "3" the User clicked on an existing bookmark.
- "4" an embedded URL.
- "5" a permanent redirect.
- "6" a temporary redirect.

URLs are maintained in the "moz_places" table under the "url" column. The "visit_count" column records the number of times each site was visited and the timestamp information for a site is recorded in the "last_visit_date" column. If the User typed the URL in the address bar, a value of "1" is noted in the "typed" column.

search.sqlite

The file maintains a list of available search engines.

signons.sqlite

The file contains three tables: "moz_deleted_logins," "moz_disabledHosts," and "moz_logins." The "moz_logins" table is the repository for all the sites that a User has entered and saved their username and password. The information is usually persistent since many Users do not want to continually reenter their username and password each time they revisit the same site(s). URLs are recorded in the "hostname" column. Although usernames and passwords are encrypted and maintained in the "encryptedUsername" and "encryptedPassword" columns respectively, they may be viewable in plain text in Firefox if no Master Password has been set. The table can be imported into an existing Firefox User's profile on a forensic machine and the username and password possibly viewed by selecting "Options," from Firefox's main drop down menu, and then selecting "Security," and "Saved Passwords." When the "Saved Passwords" dialog box appears, selecting "Show Passwords" and selecting "Yes" to confirm should then display the "Site," "Username," and "Password" columns. Alternately, it may be necessary to use available decryption software to obtain the information. Time stamp information regarding when the username and password was created, last used, and last changed is stored in the "timeCreated," "timeLastUsed," and "timePasswordChanged" columns respectively. The number of times each site was visited is maintained in the "timesUsed" column.

webappstore.sqlite

The file only contains one table, “webappstore2.” Firefox uses the table for storing its Web storage objects (software methodology/protocols used for storing data in a Web browser). Web storage types consist of local and session storage (somewhat analogous to persistent and session cookies respectively). Data is usually persistent and removing history, cookies, or form information may or may not remove the data.

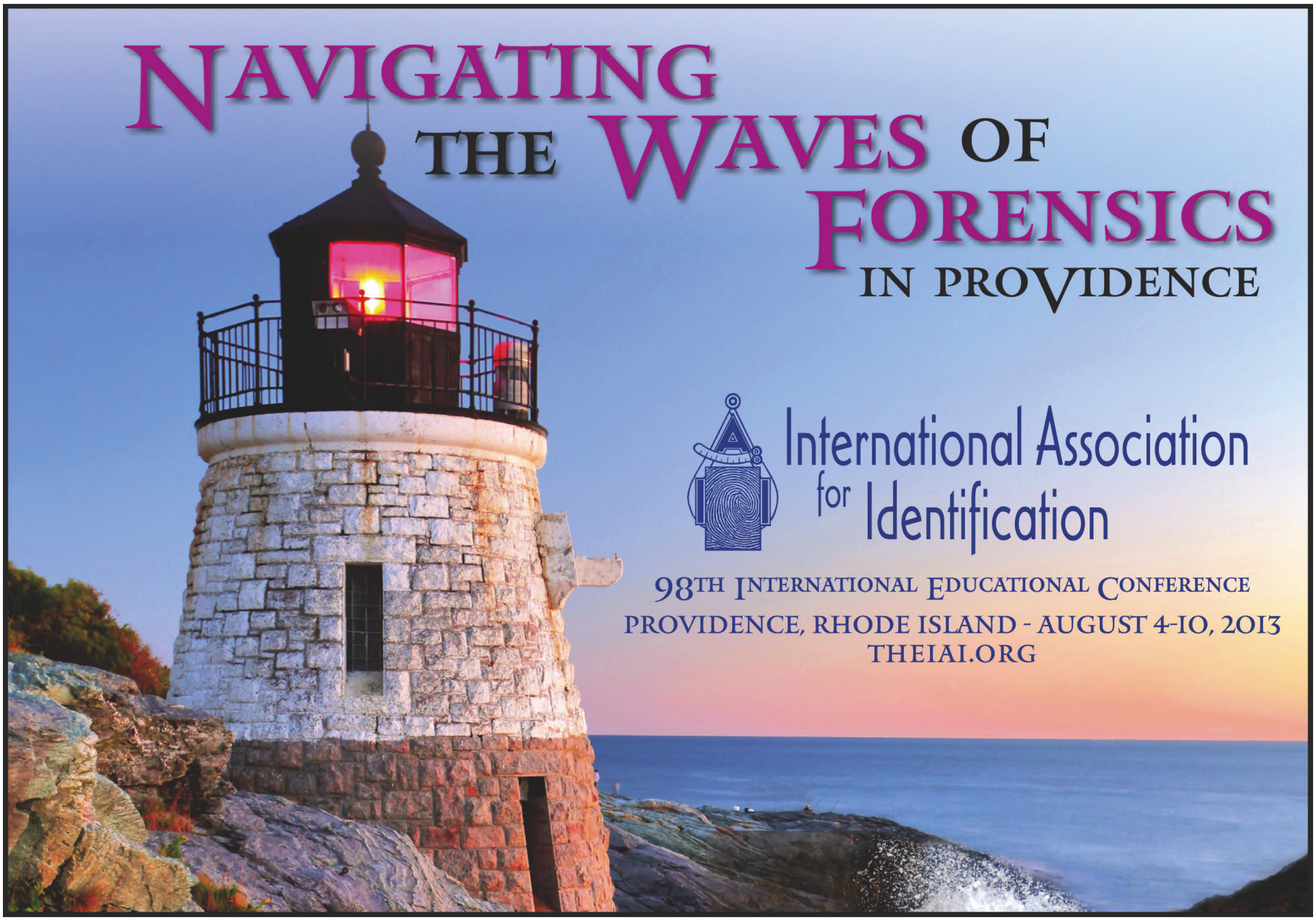
Some Caveats

Much of this discussion and any potential forensic information contained in the Firefox database files are predicated upon the fact that the User did not change certain defaults in Firefox. For instance, Firefox automatically records browsing history. However, a User can browse the Internet and prevent Firefox from storing certain information by selecting the “Start Private Browsing” option from the main drop down menu. For that session, no additional data will be recorded in the history menu, no new passwords will be saved, no downloaded files will be listed in the downloads window, no data from forms filled out online will be saved, no cookies will be stored, any files opened in external applications will be cleared from the temporary folder, and no cached files will be saved. Any new bookmarks created, however, will remain. Most of this information would normally be stored in the various database files previously discussed. (Note: selecting this feature does not make a User anonymous. The sites visited and/or the IP provider can still track User activity).

Alternately, a User can permanently prevent Firefox from recording browsing history by selecting “Options” from Firefox’s main drop down menu and selecting the “Privacy” tab. The default is to “Remember history” and options are provided to manually “clear your recent history” and “remove individual cookies.” If the User selects the second option, “Never remember history,” Firefox will no longer record site visits and provides the User with the option to “clear all current history.” Additionally, a User can select a third option, “Use custom settings for history,” and then check “Always use private browsing mode” to prevent Firefox from tracking browsing history.

If the User manually chooses to clear all browsing history, then potentially valuable forensic information may be lost from many of the previously discussed database files. Fortunately for investigators, for convenience purposes, the overwhelming number of Users do not select the “Start Private Browsing” or the “Never remember history” options. Nor do they clear their history or cookies.

John J. Barbara *owns Digital Forensics Consulting, LLC, providing consulting services for companies and laboratories seeking digital forensics accreditation. jjb@digforcon.com*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VPP, OSHA's Voluntary Protection Program: Part 1

OSHA's Safety Management Program

There is a definite and proven link between strong and efficient health and safety management and reduced occupational injuries and illnesses. A robust health and safety management program can benefit any workplace no matter how large or small. Recognizing this, OSHA developed an assistance program called VPP for Voluntary Protection Program. This first in a two part series describes how this program came about and its essential elements.

OSHA celebrated its 40th birthday in 2011 and to commemorate the milestone, the Assistant Secretary of Labor, Dr. David Michaels, gave some excellent remarks at the Center for American Progress in April.[1] The Occupational Safety and Health Act created by President Nixon and the Congress forty years ago recognized that workers deserve work places free of hazards and that many workplace injuries, illnesses, and fatalities are preventable and not just "Acts of God." President Nixon described the Occupational Safety and Health Act as "…one of the most important pieces of legislation…ever passed…" Dr. Morton Corn, appointed as Secretary of Labor by President Ford, went even further stating the OSH Act was "…a new right in the Bill of Rights—a right to a safe and healthful workplace."

The take-away message for us from Dr. Michaels' remarks: the evidence is in and OSHA has made significant strides in ensuring all workers have the basic human right to a safe workplace. Consider these statistics cited by Dr. Michaels:

- Worker deaths are down from about 14,000 in 1970 to 4,400 in 2009.
- Reported injuries and illnesses are down from 10.9 incidents per 100 workers in 1972 to fewer than 4 in 2009.
- Worker exposures to asbestos, lead, and benzene have been dramatically reduced following enactment of specific OSHA standards in recent years.

Clearly, progress has occurred. But, 4,400 worker deaths are still way too many, more than twelve deaths per day. We can and must continue to do better. Because, for one, in addition to these deaths there are more than 3 million workers that suffer serious job-related injuries each year and many thousands more that develop serious job-related illnesses. Injuries and illnesses that can destroy families financially and in many other ways.

Now the big question: How do we keep moving forward, improving working conditions and workplace safety? First, we have to admit that on-the-job injuries, illnesses, and deaths are preventable. Preventable by using basic safety precautions such as preventing falls, eliminating hazards and exposures, and guarding equipment and machinery. In other words, preventable by just following existing OSHA safety standards. As Dr. Michaels' stated "OSHA doesn't kill jobs; it stops jobs from killing people."

Much More than Enforcement

We must not think of OSHA as "the enforcer" with its only purpose being to levy hefty fines when we are caught doing things wrong. OSHA is a resource, one that can help in big ways. In fact, one OSHA service provides free information and assistance to small businesses before they are cited for violations, making more than 30,000 on-site visits each year. If you feel you have hit a wall give them a call.

More than twenty years ago OSHA first issued voluntary Safety and Health Program Management Guidelines.[2] Recognizing that a strong correlation exists between sound and effective safety and health management and a low incidence of occupational illnesses and injuries, OSHA released general guidelines to help businesses and employers to develop systematic policies, procedures, and practices to protect employees from job-related safety and health hazards. These voluntary safety management guidelines incorporate four general principles:

- Encourage employers to implement and maintain policies and practices that recognize and protect employees from occupational safety and health hazards.

- Effective programs are able to identify, evaluate, and prevent or control general workplace hazards, specific job hazards, and foreseeable potential hazards.
- Effective programs look beyond specific regulatory requirements and address all hazards whether or not compliance is at issue.
- Effective practice is more important than the extent of written programs, but as the size and complexity of the worksite increase, so do the hazards and written guidance is needed to make sure communication of policies is clear and implementation is fair and consistent.

At the heart of the voluntary safety management program are four major elements that define an effective program. Based on the cumulative evidence, systematic policies and practices are fundamental in reducing work-related illnesses and injuries and their associated high economic costs including workers' compensation, insurance, and medical services. Ensuring your program incorporates these four elements will strengthen safety and health efforts and aid its success.

- **Management commitment and employee involvement.** Management commitment is the motivating force for the business or organization and provides the resources necessary to implement the programs. Commitment by management tells workers that their safety and health are valuable and important to the organization. Employee involvement is paramount and provides a way for workers to take responsibility for protection of safety and health for themselves and their fellow workers.
- **Workplace and job hazard analysis.** An effective management program actively examines the worksite and specific jobs to anticipate and prevent unsafe conditions. Regular analysis identifies existing hazards as well as operations that might create new ones.
- **Prompt implementation of hazard prevention and controls.** Once a hazard or potential hazard is found or recognized, elimination or controls are undertaken in a timely manner. Engineering controls, design, or re-design are implemented first where feasible. Where engineering solutions to eliminate the hazard are not feasible, controls are put in place to reduce the exposure hazards and prevent unsafe conditions.
- **Health and safety training.** Comprehensive training is tailored to the size and complexity of the facility and the nature of the hazards. Safety training addresses responsibilities of all personnel and is best when tied to job practices and performance requirements.

In the next issue we will complete this two part series on OSHA's VPP with details of the program and examples of successes. Until then we encourage you to give VPP and, more importantly, proactive safety, some thought.

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Investigating Beyond the Fender Bender

Most of the time traffic accidents are fairly standard—the typical fender bender where one person runs into another. But sometimes officers deal with much more serious, complex situations. Dealing with a hundred car pile-up, for example, is quite challenging, since it's like carrying out multiple investigations simultaneously.

Because this type of case usually involves extensive damage to property, serious injuries, and/or fatalities, lawsuits will likely result. Questions of liability, product failure, etc. will also come up. Since the CSO's responsibilities include documentation, evidence identification, and evidence collection, we'll look at each of those areas.

Documentation

One of the most important aspects of traffic investigation is proper documentation. By observing the scene as a whole, you'll understand it, determine what actions need to be taken, and identify the areas to search for evidence.

Photography

Photograph the scene completely. Include overview, mid-range, and close-up shots. Video may also be useful. Occasionally, aerial photography may be needed.

I had a case where a guy hit a girl on a bicycle. The girl broke the windshield, hit the roof, broke the back wiper blade, and then landed in the middle of the road. The driver continued on—with the bicycle attached to the front of the vehicle—for another 1.9 miles. We photographed all aspects of the scene, including damage to the bumper, skid marks, and street markings. The evidence indicated that the driver crossed the white line and was nearly off the road at impact. We used aerial photography to document the scene, beginning with the impact point and including all 1.9 miles the driver traveled. In court, we used all of the photos to show what happened.

Diagrams

Careful diagramming can help explain the scene. Each diagram should be clearly labeled with relevant information such as the case number, date and time of accident, location (name of street/road/highway), orientation (North), landmarks, etc. Also indicate the location of the vehicle(s); victim(s); and evidence such as skid marks, debris, broken glass, etc. Also show obstructions or other problems.

Replicating Events

Sometimes you need to replicate important elements of the event. For example, I investigated another fatality involving a girl on a bicycle. This time, however, the driver crested a hill while the sun was setting. To see if the sun was a factor, we returned to the scene and crested the hill at the same time of day, videotaping the whole process. By replicating the event, we discovered that the driver was sun blinded when he crested the hill. In other cases, road conditions, weather, lighting, etc. may also be relevant to determining fault.

Evidence Identification and Collection

As with any case you work, finding and collecting evidence are essential. Always document where you find evidence, and photograph it before removing it. The most important source of evidence is usually the vehicle involved. Once the scene is processed and documented, the vehicle can be taken to the proper facility for processing. Before it's moved, check for alcohol, guns and other weapons, drugs, stolen property, etc.

Important evidence may also be scattered throughout the scene. Check for debris, skid marks, broken glass, gasoline, oil, blood, and items that may belong to the victim. Evidence may be on the side of the road, in adjacent ditches, etc., so pay attention to the surrounding areas.

With questions about fault and product failure, specific evidence is important. For example, in the case of the sun blinded driver, we examined the bottom of his shoe and matched the pattern we found to the brake pedal, proving that he hit the brake and tried to stop. In another case I worked, a person drove into a bridge pillar at a high rate of speed. Were the brakes faulty? Was there some other kind of mechanical failure? Driver error? Again, we examined the bottom of the driver's shoe. This time, we found the unique pattern of the accelerator transferred to the shoe, proving the driver had committed suicide.

Traffic investigations can be overwhelming. But no matter the situation, the key is to follow your training. Also remember that at a traffic scene, you're part of a joint venture. You and the other officers and specialists all bring unique skills to the job; your combined efforts make for a better investigation.

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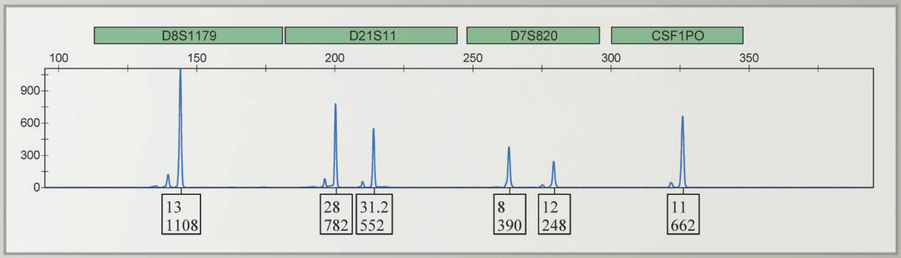

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